

**SECRET**

(i) APPLICANT: SANTEN PHARMACEUTICAL CO., LTD.

(iii) NUMBER OF SEQUENCES: 2

(A) ADDRESSEE: SANTEN PHARMACEUTICAL CO., LTD.

(B) STREET: 9 ? 19 Shimoshinjo 3-chome Higashiyodogawa-Ku

(C) CITY: Osaka

(D) STATE: Osaka

(E) COUNTRY: JAPAN

(F) ZIP: 533-0021

(A) MEDIUM TYPE: Diskette, 3.5 inch, 1.44 MB, storage

(B) COMPUTER: IBM PS/2 or compatibles

(C) OPERATING SYSTEM: WINDOWS 95/97

(D) SOFTWARE: Microsoft Word 97

(A) APPLICATION NUMBER: 09/381,810

(C) CLASSIFICATION: 435

(A) APPLICATION NUMBER: JP09 094845

(B) FILING DATE: 28-MAR-1997

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Burton A. Amernick

(B) REGISTRATION NUMBER: 24852

(C) REFERENCE/DOCKET NUMBER: 1581/00156

(ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: (202) 331-7111

(B) FAX: (202) 293-6229

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH F342 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY F linear

(ii) MORECULE TYPE F peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

Met Val Gln Ala Ser Gly His Arg Arg Ser Thr Arg Gly Ser Lys Met  
5 10 15

Val Ser Trp Ser Val Ile Ala Lys Ile Gln Glu Ile Leu Gln Arg Lys

Met Val Arg Glu Phe Leu Ala Glu Phe Met Ser Thr Tyr Val Met Met

Val Phe Gly Leu Gly Ser Val Ala His Met Val Leu Asn Lys Lys Tyr  
50 55 60

Gly Ser Tyr Leu Gly Val Asn Leu Gly Phe Gly Phe Gly Val Thr Met  
65 70 75 80

Gly Val His Val Ala Gly Arg Ile Ser Gly Ala His Met Asn Ala Ala  
85 90 95

Val Thr Phe Ala Asn Cys Ala Leu Gly Arg Val Pro Trp Arg Lys Phe

	100		105		110										
Pro	Val	Tyr	Val	Leu	Gly	Gln	Phe	Leu	Gly	Ser	Phe	Leu	Ala	Ala	Ala
	115						120					125			
Thr	Ile	Tyr	Ser	Leu	Phe	Tyr	Thr	Ala	Ile	Leu	His	Phe	Ser	Gly	Gly
	130						135					140			
Gln	Leu	Met	Val	Thr	Gly	Pro	Val	Ala	Thr	Ala	Gly	Ile	Phe	Ala	Thr
145					150					155					160
Tyr	Leu	Pro	Asp	His	Met	Thr	Leu	Trp	Arg	Gly	Phe	Leu	Asn	Glu	Ala
			165						170					175	
Trp	Leu	Thr	Gly	Met	Leu	Gln	Leu	Cys	Leu	Phe	Ala	Thr	Thr	Asp	Gln
		180						185					190		
Glu	Asn	Asn	Pro	Ala	Leu	Pro	Gly	Thr	Glu	Ala	Leu	Val	Ile	Gly	Ile
	195						200					205			
Leu	Val	Val	Ile	Ile	Gly	Val	Ser	Leu	Gly	Met	Asn	Thr	Gly	Tyr	Ala
	210					215					220				
Ile	Asn	Pro	Ser	Arg	Asp	Leu	Pro	Pro	Arg	Ile	Phe	Thr	Phe	Ile	Ala
225					230					235					240
Gly	Trp	Gly	Lys	Gln	Val	Phe	Ser	Asn	Gly	Glu	Asn	Trp	Trp	Trp	Val
			245						250					255	
Pro	Val	Val	Ala	Pro	Leu	Leu	Gly	Ala	Tyr	Leu	Gly	Gly	Ile	Ile	Tyr
		260						265					270		
Leu	Val	Phe	Ile	Gly	Ser	Thr	Ile	Pro	Arg	Glu	Pro	Leu	Lys	Leu	Glu
	275						280					285			
Asp	Ser	Val	Ala	Tyr	Glu	Asp	His	Gly	Ile	Thr	Val	Leu	Pro	Lys	Met
	290					295					300				
Gly	Ser	His	Glu	Pro	Thr	Ile	Ser	Pro	Leu	Thr	Pro	Val	Ser	Val	Ser
305					310					315					320
Pro	Ala	Asn	Arg	Ser	Ser	Val	His	Pro	Ala	Pro	Pro	Leu	His	Glu	Ser
			325					330						335	
Met	Ala	Leu	Glu	His	Phe										
		340													

(2) INFORMATION FOR SEQ ID No F2

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH F1258 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY F linear

(ii) MOLECULE TYPE: cDNA to mRNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens
- (B) TISSUE TYPE: fat tissue

(ix) FEATURE:

- (A) NAME/KEY: exon
- (B) LOCATION F173..1198
- (C) IDENTIFICATION METHOD: by experiment

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

GGCTCTGGAC	TGGGGACACA	GGGATAGCTG	AGCCCCAGCT	GGGGGTGGAA	GCTGAGCCAG	60
GGACAGTCAC	GGAGGAACAA	GATCAAGATG	CGCTGTAAC	GAGAAGCCCC	CAAGGCGGAG	120
GCTGAGAATC	AGAGACATTT	CAGCAGACAT	CTACAAATCT	GAAAGACAAA	AC ATG GTT	178
					Met Val	
					1	
CAA GCA TCC	GGG CAC AGG	CGG TCC ACC	CGT GGC TCC	AAA ATG GTC	TCC	226
Gln Ala Ser	Gly His Arg	Arg Ser Thr	Arg Gly Ser	Lys Met Val	Ser	
5		10		15		

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TGG TCC GTG ATA GCA AAG ATC CAG GAA ATA CTG CAG AGG AAG ATG GTG	274
Trp Ser Val Ile Ala Lys Ile Gln Glu Ile Leu Gln Arg Lys Met Val	
20 25 30	
CGA GAG TTC CTG GCC GAG TTC ATG AGC ACA TAT GTC ATG ATG GTA TTC	322
Arg Glu Phe Leu Ala Glu Phe Met Ser Thr Tyr Val Met Met Val Phe	
35 40 45 50	
GGC CTT GGT TCC GTG GCC CAT ATG GTT CTA AAT AAA AAA TAT GGG AGC	370
Gly Leu Gly Ser Val Ala His Met Val Leu Asn Lys Lys Tyr Gly Ser	
55 60 65	
TAC CTT GGT GTC AAC TTG GGT TTT GGC TTC GGA GTC ACC ATG GGA GTG	418
Tyr Leu Gly Val Asn Leu Gly Phe Gly Phe Gly Val Thr Met Gly Val	
70 75 80	
CAC GTG GCA GGC CGC ATC TCT GGA GCC CAC ATG AAC GCA GCT GTG ACC	466
His Val Ala Gly Arg Ile Ser Gly Ala His Met Asn Ala Ala Val Thr	
85 90 95	
TTT GCT AAC TGT GCG CTG GGC CGC GTG CCC TGG AGG AAG TTT CCG GTC	514
Phe Ala Asn Cys Ala Leu Gly Arg Val Pro Trp Arg Lys Phe Pro Val	
100 105 110	
TAT GTG CTG GGG CAG TTC CTG GGC TCC TTC CTG GCG GCT GCC ACC ATC	562
Tyr Val Leu Gly Gln Phe Leu Gly Ser Phe Leu Ala Ala Ala Thr Ile	
115 120 125 130	
TAC AGT CTC TTC TAC ACG GCC ATT CTC CAC TTT TCG GGT GGA CAG CTG	610
Tyr Ser Leu Phe Tyr Thr Ala Ile Leu His Phe Ser Gly Gly Gln Leu	
135 140 145	
ATG GTG ACC GGT CCC GTC GCT ACA GCT GGC ATT TTT GCC ACC TAC CTT	658
Met Val Thr Gly Pro Val Ala Thr Ala Gly Ile Phe Ala Thr Tyr Leu	
150 155 160	
CCT GAT CAC ATG ACA TTG TGG CGG GGC TTC CTG AAT GAG GCG TGG CTG	706
Pro Asp His Met Thr Leu Trp Arg Gly Phe Leu Asn Glu Ala Trp Leu	
165 170 175	
ACC GGG ATG CTC CAG CTG TGT CTC TTC GCC ATC ACG GAC CAG GAG AAC	754
Thr Gly Met Leu Gln Leu Cys Leu Phe Ala Thr Thr Asp Gln Glu Asn	
180 185 190	
AAC CCA GCA CTG CCA GGA ACA GAG GCG CTG GTG ATA GGC ATC CTC GTG	802
Asn Pro Ala Leu Pro Gly Thr Glu Ala Leu Val Ile Gly Ile Leu Val	
195 200 205 210	
GTC ATC ATC GGG GTG TCC CTT GGC ATG AAC ACA GGA TAT GCC ATC AAC	850
Val Ile Ile Gly Val Ser Leu Gly Met Asn Thr Gly Tyr Ala Ile Asn	
215 220 225	
CCG TCC CGG GAC CTG CCC CCC CGC ATC TTC ACC TTC ATT GCT GGT TGG	898
Pro Ser Arg Asp Leu Pro Pro Arg Ile Phe Thr Phe Ile Ala Gly Trp	
230 235 240	
GGC AAA CAG GTC TTC AGC AAT GGG GAG AAC TGG TGG TGG GTG CCA GTG	946
Gly Lys Gln Val Phe Ser Asn Gly Glu Asn Trp Trp Trp Val Pro Val	
245 250 255	
GTG GCA CCA CTT CTG GGT GCC TAT CTA GGT GGC ATC ATC TAC CTG GTC	994
Val Ala Pro Leu Leu Gly Ala Tyr Leu Gly Gly Ile Ile Tyr Leu Val	
260 265 270	
TTC ATT GGC TCC ACC ATC CCA CGG GAG CCC CTG AAA TTG GAG GAT TCT	1042
Phe Ile Gly Ser Thr Ile Pro Arg Glu Pro Leu Lys Leu Glu Asp Ser	
275 280 285 290	
GTG GCG TAT GAA GAC CAC GGG ATA ACC GTA TTG CCC AAG ATG GGA TCT	1090
Val Ala Tyr Glu Asp His Gly Ile Thr Val Leu Pro Lys Met Gly Ser	
295 300 305	
CAT GAA CCC ACG ATC TCT CCC CTC ACC CCC GTC TCT GTG AGC CCT GCC	1138
His Glu Pro Thr Ile Ser Pro Leu Thr Pro Val Ser Val Ser Pro Ala	
310 315 320	

AAC AGA TCT TCA GTC CAC CCT GCC CCA CCC TTA CAT GAA TCC ATG GCC 1186  
 Asn Arg Ser Ser Val His Pro Ala Pro Pro Leu His Glu Ser Met Ala  
 325 330 335  
 CTA GAG CAC TTC TAAGCAGAGA TTATTTGTGA TCCCATCCAT TCCCAATAA 1238  
 Leu Glu His Phe  
 340  
 AGCAAGGCTT GTCCGACAAA 1258

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